What is claimed is:

1. A method for assigning a cellular function to a component of a biochemical system, comprising:

(a) determining a multidimensional shape space for one or more components of a biochemical system in a reference state;

(b) perturbing a component within said biochemical system;

(c) determining a perturbed multidimensional shape space for one or more components of a pathway in said perturbed biochemical system, and

(d) identifying a multidimensional coordinate point corresponding to a component of said perturbed pathway altered between reference and perturbed multidimensional shape spaces, said identified component being assigned a cellular function of said perturbed pathway.

2. The method of claim 1, further comprising perturbing a second component of said perturbed pathway and determining a multidimensional coordinate point for said identified component, wherein an alteration in said multidimensional coordinate point for said identified component confirms the assignment of said identified component to said perturbed pathway.

3. The method of claim 1, wherein said biochemical system is selected from the group consisting of a cell, tissue, organism and subcellular system.

4. The method of claim 1, wherein said multidimensional shape space comprises multidimensional coordinate points representing expression data elements.

5. The method of claim 1, further comprising determining a multidimensional shape space for at least two perturbed pathways.

6. The method of claim 1, further comprising determining a multidimensional shape space for at three perturbed pathways

7. The method of claim 1, further comprising determining a multidimensional shape space for substantially all perturbed pathways of said biochemical system.

8. A method for assigning a cellular function to a component of a biochemical system, comprising:

(a) determining an integrated multidimensional data space for each of at least two networks in a reference state biochemical system;

(b) determining a multidimensional shape space for at least one network in a perturbed state biochemical system, and

(c) determining a component multidimensional coordinate point contained within a multidimensional shape space representing the difference between multidimensional data spaces of reference and perturbed states of said biochemical system, said component being linked to said network having perturbed multidimensional shape space, and thereby being assigned the cellular function of said network.

9. The method of claim 8, further comprising determining a multidimensional shape space for at least one pathway in a perturbed state biochemical system, and determining a component multidimensional coordinate point contained within a multidimensional shape space representing the difference between multidimensional data spaces of reference and perturbed states of said biochemical system, said component being linked to said pathway having perturbed multidimensional shape space, and thereby being assigned the cellular function of said pathway.

10. The method of claim 8, wherein said biochemical system is selected from the group consisting of a cell, tissue, organism and subcellular system.

11. The method of claim 8, wherein said multidimensional shape space comprises multidimensional coordinate points representing a data element selected from the group consisting of nucleic acid expression data element and polypeptide expression data element.

12. The method of claim 8, further comprising determining an integrated multidimensional shape space for at least three networks.

13. The method of claim 8, further comprising determining a multidimensional shape space for at least four networks.

14. The method of claim 8, further comprising determining a multidimensional shape space for substantially all networks of said biochemical system.

15. The method of claim 8, further comprising determining a multidimensional shape space for at least two networks in a perturbed state biochemical system.

16. A method for assigning a cellular function to a component of a biochemical system, comprising:

(a) comparing two integrated multidimensional data spaces of a biochemical system obtained in reference and perturbed states of a biochemical system, said integrated multidimensional data spaces comprising at least two networks, and

(b) determining a component multidimensional coordinate point contained within a multidimensional data space representing the difference between multidimensional data spaces of reference and perturbed states of said biochemical system, said component being linked to said network having said perturbed multidimensional shape space, and thereby being assigned a cellular function of said network.

17. The method of claim 16, further comprising determining two or more pathway components, each having multidimensional coordinate points altered between said reference and perturbed states of said biochemical system, and linking a component having multidimensional coordinate points altered between said reference and perturbed states to said pathway components, thereby assigning to said component a cellular function of said pathway.

18. The method of claim 16, wherein said biochemical system is selected from the group consisting of a cell, tissue, organism and subcellular system.

19. The method of claim 16, wherein said integrated multidimensional data spaces comprise at least three networks.

20. The method of claim 16, further comprising determining a multidimensional shape space for at least four networks.

21. The method of claim 16, further comprising determining a multidimensional shape space for substantially all networks of said biochemical system.

22. A method for assigning a cellular function to a component of a biochemical system, comprising:

(a) perturbing a component of a network in a reference biochemical system;

(b) determining a multidimensional coordinate point representing a data element of one or more components of a perturbed biochemical system;

(c) comparing said multidimensional coordinate point to a reference data element region, and

(d) determining if said multidimensional coordinate point is within or outside said reference data element region, wherein a multidimensional coordinate point outside of said reference data element region indicates that said component is linked to said perturbed biochemical network, and is thereby assigned a cellular function of said network.

23. The method of claim 22, wherein said data element is a data element selected from the group consisting of nucleic acid expression element and polypeptide expression element.

24. A method for assigning a cellular function to a component of a biochemical system, comprising:

(a) determining a multidimensional coordinate point representing a data element of a set of components in a biochemical network of a perturbed biochemical system;

(b) comparing said multidimensional coordinate point to a network-associated reference expression region of said set of components, and

(c) determining if said multidimensional coordinate point is outside of said network-associated reference expression region, wherein a multidimensional coordinate point outside of said network-associated reference expression region indicates a perturbed state of said network, said component being linked to said perturbed network and thereby being assigned a cellular function of said network.

25. The method of claim 24, wherein said biochemical system is selected from the group consisting of a cell, tissue, organism and subcellular system.

26. The method of claim 24, wherein said data element is an expression data element.

27. The method of claim 24, wherein said reference expression region indicates a normal state of a biochemical system.

28. The method of claim 24, wherein said components of the biochemical network comprise nucleic acids.

29. The method of claim 24, wherein said components of the biochemical network comprise polypeptides.

30. A method for assigning a cellular function to a component of a biochemical system, comprising:

(a) determining a multidimensional coordinate point representing a data element of a set of components in a biochemical pathway of a perturbed biochemical system;

(b) comparing said multidimensional coordinate point to a pathway-associated reference expression region of said set of components, and

(c) determining if said multidimensional coordinate point is outside of said pathway-associated reference expression region, wherein a multidimensional coordinate point outside of said pathway-associated reference expression region indicates a perturbed state of said pathway, said component being linked to said perturbed pathway and thereby being assigned a cellular function of said pathway.

31. The method of claim 30, wherein said biochemical system is selected from the group consisting of a cell, tissue, organism and subcellular system.

32. The method of claim 30, wherein said data element is an expression data element.

33. The method of claim 30, wherein said reference expression region indicates a normal state of a biochemical system.

34. The method of claim 30, wherein said components of the biochemical network comprise nucleic acids.

35. The method of claim 30, wherein said components of the biochemical network comprise polypeptides.

36. A method for identifying a component of a biochemical network, comprising:

(a) determining an integrated multidimensional data space for a biochemical system comprising at least two networks;

(b) perturbing at least one component of a biochemical pathway, and

(c) determining a multidimensional coordinate point for a candidate network component affected by said perturbing of the biochemical system, wherein a candidate component having an altered multidimensional coordinate point in response to said perturbation is identified as a component of said biochemical network.

37. The method of claim 36, wherein said biochemical system is selected from the group consisting of a cell, tissue, organism and subcellular system.

38. The method of claim 36, further comprising determining an integrated multidimensional data space for a biochemical system comprising at least three networks.

39. The method of claim 36, further comprising perturbing at least two components of a biochemical pathway.

40. The method of claim 36, wherein said multidimensional coordinate point for a candidate network component represents a data element selected from the group consisting of nucleic acid expression data element and protein expression data element.

41. The method of claim 36, wherein said network further comprises two or more pathways.

42. A method for identifying functionally interactive components of a biochemical network, comprising:

(a) determining a set of components of a biochemical system, each component linked to another by a common first data element;

(b) determining a set of components of a biochemical system linked by a common second data element, the second data element represented by a multidimensional coordinate point corresponding to each component, and

(c) integrating the set of components linked by a common first data element with the set of components linked by a common second data element represented by a multidimensional coordinate point corresponding to each component, to produce a network of functionally interactive components, each component within said network of functionally interactive components being characterized as linked by at least two data elements.

43. The method of claim 42, wherein said biochemical system is selected from the group consisting of a cell, tissue, organism and subcellular system.

44. The method of claim 42, wherein said first data element is selected from the group consisting of physical interaction data element and polypeptide expression data element.

45. The method of claim 42, wherein said second data element is selected from the group consisting of polypeptide expression data element and nucleic acid expression data element.

46. The method of claim 42, wherein each component within said network of functionally interactive components being characterized as linked by at least three data elements.

47. A method for identifying a compound that restores a biochemical system to a reference state, comprising:

(a) determining an integrated multidimensional data space for a reference state of a biochemical system;

(b) determining an integrated multidimensional data space for a perturbation state of a biochemical system;

(c) contacting a biochemical system exhibiting the perturbation state with a test compound;

(d) determining a multidimensional shape space for said biochemical system contacted with said test compound, and

(e) identifying a compound that restores at least two multidimensional coordinate points in said perturbed multidimensional data space to reference state conditions, said compound having the ability to restore a biochemical system to a reference state.

48. The method of claim 47, wherein said biochemical system is selected from the group consisting of a cell, tissue, organism and subcellular system.

49. The method of claim 47, wherein said perturbation state of a biochemical system is a pathological condition.